

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/155,514E
Source: 1Fw/6
Date Processed by STIC: 9/12/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/12/2005

PATENT APPLICATION: US/09/155,514E

TIME: 09:41:26

Input Set : A:\1102-98.txt

Output Set: N:\CRF4\09122005\I155514E.raw

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4 <110> APPLICANT: Kainoh, Mie
5      Tanaka, Toshiaki
7 <120> TITLE OF INVENTION: Chimeric Proteins, their Heterodimer
8      Complexes, and Platelet Substitutes
12 <130> FILE REFERENCE: 1102-98
14 <140> CURRENT APPLICATION NUMBER: 09/155,514E
15 <141> CURRENT FILING DATE: 1998-11-17
17 <150> PRIOR APPLICATION NUMBER: WO PCT/JP98/00370
18 <151> PRIOR FILING DATE: 1998-01-29
20 <150> PRIOR APPLICATION NUMBER: JP 9-15118
21 <151> PRIOR FILING DATE: 1997-01-29
23 <150> PRIOR APPLICATION NUMBER: JP-9-234544
24 <151> PRIOR FILING DATE: 1997-08-29
26 <160> NUMBER OF SEQ ID NOS: 34
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 4228
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: sequence encoding fusion protein
W--> 38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)...(2958)
W--> 41 <221> CDS
42 <222> LOCATION: (3316)...(3360)
W--> 44 <221> CDS
45 <222> LOCATION: (3479)...(3808)
W--> 47 <221> CDS
48 <222> LOCATION: (3905)...(4228)
W--> 50 <400> 1
51 atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg      48
52 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
53 1          5          10          15
55 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg      96
56 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
57          20          25          30
59 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg      144
60 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
61          35          40          45
63 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg      192
64 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
65          50          55          60
67 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc      240

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68 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
69 65 70 75 80
71 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga 288
72 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
73 85 90 95
75 tgc agg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg 336
76 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
77 100 105 110
79 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga 384
80 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
81 115 120 125
83 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat 432
84 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
85 130 135 140
87 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata 480
88 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
89 145 150 155 160
91 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct 528
92 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
93 165 170 175
95 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat 576
96 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
97 180 185 190
99 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata 624
100 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
101 195 200 205
103 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca 672
104 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
105 210 215 220
107 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa 720
108 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
109 225 230 235 240
111 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat 768
112 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
113 245 250 255
115 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc 816
116 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
117 260 265 270
119 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat 864
120 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
121 275 280 285
123 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa 912
124 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
125 290 295 300
127 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgt gct gtg gac 960
128 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
129 305 310 315 320
131 ctc aat gca gat ggc ttc tca gat ctg ctc gga gca ccc atg cag 1008
132 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln

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133		325		330		335		
135	agc acc atc	aga gag gaa gga	aga gtg ttt gtg	tac atc aac tct ggc	1056			
136	Ser Thr Ile	Arg Glu Glu Gly	Arg Val Phe Val Tyr	Ile Asn Ser Gly				
137		340		345		350		
139	tcg gga gca	gta atg aat gca	atg gaa aca aac	ctc gtt gga agt gac	1104			
140	Ser Gly Ala	Val Met Asn Ala	Met Glu Thr Asn	Leu Val Gly Ser Asp				
141		355		360		365		
143	aaa tat gct	gca aga ttt ggg	gaa tct ata gtt	aat ctt ggc gac att	1152			
144	Lys Tyr Ala	Ala Arg Phe Gly	Glu Ser Ile Val	Asn Leu Gly Asp Ile				
145		370		375		380		
147	gac aat gat	ggc ttt gaa gat	gtt gct atc gga	gct cca caa gaa gat	1200			
148	Asp Asn Asp	Gly Phe Glu Asp	Val Ala Ile Gly	Ala Pro Gln Glu Asp				
149	385		390		395		400	
151	gac ttg caa	ggt gct att tat	att tac aat ggc	cgt gca gat ggg atc	1248			
152	Asp Leu Gln	Gly Ala Ile Tyr	Ile Tyr Asn Gly	Arg Ala Asp Gly Ile				
153		405		410		415		
155	tcg tca acc	ttc tca cag aga	att gaa gga ctt	cag atc agc aaa tcg	1296			
156	Ser Ser Thr	Phe Ser Gln Arg	Ile Glu Gly Leu	Gln Ile Ser Lys Ser				
157		420		425		430		
159	tta agt atg	ttt gga cag tct	ata tca gga caa	att gat gca gat aat	1344			
160	Leu Ser Met	Phe Gly Gln Ser	Ile Ser Gly Gln	Ile Asp Ala Asp Asn				
161		435		440		445		
163	aat ggc tat	gta gat gta gca	gtt ggt gct ttt	cgg tct gat tct gct	1392			
164	Asn Gly Tyr	Val Asp Val Ala	Val Gly Ala Phe	Arg Ser Asp Ser Ala				
165		450		455		460		
167	gtc ttg cta	agg aca aga cct	gta gta att gtt	gac gct tct tta agc	1440			
168	Val Leu Leu	Arg Thr Arg Pro	Val Val Ile Val	Asp Ala Ser Leu Ser				
169	465		470		475		480	
171	cac cct gag	tca gta aat aga	acg aaa ttt gac	tgt gtt gaa aat gga	1488			
172	His Pro Glu	Ser Val Asn Arg	Thr Lys Phe Asp	Cys Val Glu Asn Gly				
173		485		490		495		
175	tgg cct tct	gtg tgc ata gat	cta aca ctt tgt	ttc tca tat aag ggc	1536			
176	Trp Pro Ser	Val Cys Ile Asp	Leu Thr Leu Cys	Phe Ser Tyr Lys Gly				
177		500		505		510		
179	aag gaa gtt	cca ggt tac att	gtt ttg ttt tat	aac atg agt ttg gat	1584			
180	Lys Glu Val	Pro Gly Tyr Ile	Val Leu Phe Tyr	Asn Met Ser Leu Asp				
181		515		520		525		
183	gtg aac aga	aag gca gag tct	cca cca aga ttc	tat ttc tct tct aat	1632			
184	Val Asn Arg	Lys Ala Glu Ser	Pro Pro Arg Phe	Tyr Phe Ser Ser Asn				
185		530		535		540		
187	gga act tct	gac gtg att aca	gga agc ata cag	gtg tcc agc aga gaa	1680			
188	Gly Thr Ser	Asp Val Ile Thr	Gly Ser Ile Gln	Val Ser Ser Arg Glu				
189	545		550		555		560	
191	gct aac tgt	aga aca cat caa	gca ttt atg cgg	aaa gat gtg cgg gac	1728			
192	Ala Asn Cys	Arg Thr His Gln	Ala Phe Met Arg	Lys Asp Val Arg Asp				
193		565		570		575		
195	atc ctc acc	cca att cag att	gaa gct gct tac	cac ctt ggt cct cat	1776			
196	Ile Leu Thr	Pro Ile Gln Ile	Glu Ala Tyr His	Leu Gly Pro His				
197		580		585		590		

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199 gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att 1824
200 Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile
201      595      600      605
203 ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt 1872
204 Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe
205      610      615      620
207 gca agg ttt tgt gcc cat gaa aat tgt tct gct gat tta cag gtt tct 1920
208 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser
209 625      630      635      640
211 gca aag att ggg ttt ttg aag ccc cat gaa aat aaa aca tat ctt gct 1968
212 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala
213      645      650      655
215 gtt ggg agt atg aag aca ttg atg ttg aat gtg tcc ttg ttt aat gct 2016
216 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala
217      660      665      670
219 gga gat gat gca tat gaa acg act cta cat gtc aaa cta ccc gtg ggt 2064
220 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly
221      675      680      685
223 ctt tat ttc att aag att tta gag ctg gaa gag aag caa ata aac tgt 2112
224 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys
225      690      695      700
227 gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc 2160
228 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly
229 705      710      715      720
231 tat ata tat gta gat cat ctc tca agg ata gat att agc ttt ctc ctg 2208
232 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu
233      725      730      735
235 gat gtg agc tca ctc agc aga gcg gaa gag gac ctc agt atc aca gtg 2256
236 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val
237      740      745      750
239 cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc 2304
240 His Ala Thr Cys Glu Asn Glu Glu Met Asp Asn Leu Lys His Ser
241      755      760      765
243 aga gtg act gta gca ata cct tta aaa tat gag gtt aag ctg act gtt 2352
244 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val
245      770      775      780
247 cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa 2400
248 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu
249 785      790      795      800
251 aat gag cct gaa acg tgc atg gtg gag aaa atg aac tta act ttc cat 2448
252 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His
253      805      810      815
255 gtt atc aac act ggc aat agt atg gct ccc aat gtt agt gtg gaa ata 2496
256 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile
257      820      825      830
259 atg gta cca aat tct ttt agc ccc caa act gat aag ctg ttc aac att 2544
260 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile
261      835      840      845
263 ttg gat gtc cag act act act gga gaa tgc cac ttt gaa aat tat caa 2592

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264 Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
265      850                      855                      860
267 aga gtg tgt gca tta gag cag caa aag agt gca atg cag acc ttg aaa 2640
268 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
269 865                      870                      875                      880
271 ggc ata gtc cgg ttc ttg tcc aag act gat aag agg cta ttg tac tgc 2688
272 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
273                      885                      890                      895
275 ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa 2736
276 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
277                      900                      905                      910
279 atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg 2784
280 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
281                      915                      920                      925
283 cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata 2832
284 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
285                      930                      935                      940
287 aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac 2880
288 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
289 945                      950                      955                      960
291 aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa 2928
292 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
293                      965                      970                      975
295 aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaag caggctcagc 2978
296 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu
297                      980                      985
299 gctcctgcct ggacgcatcc cggctatgca gccccagtcc agggcagcaa ggcaggcccc 3038
300 gtctgcctct tcacccggag cctctgcccc cccactcat gctcaggag agggctcttct 3098
301 ggctttttcc caggctctgg gcaggcacag gctaggtgcc cctaaccag gccctgcaca 3158
302 caaaggggca ggtgctgggc tcagacctgc caagagccat atccgggagg accctgcccc 3218
303 tgacctaaag ccaccccaaa ggccaaactc tccactccct cagctcggac acctctctc 3278
304 ctccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gag 3333
305                      Glu Pro Lys Ser Cys Asp
306                      990
308 aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc 3380
309 Lys Thr His Thr Cys Pro Pro Cys Pro
310                      995                      1000
312 gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcattccagg gacaggcccc 3440
313 agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa ctc ctg ggg 3496
314                      Ala Pro Glu Leu Leu Gly
315                      1005
317 gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 3544
318 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
319                      1010                      1015                      1020
321 atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 3592
322 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
323                      1025                      1030                      1035
325 gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 3640
326 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

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L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:50 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:384 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:387 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:852 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:855 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:858 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:861 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:864 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19